311

#2

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RAW SEQUENCE LISTING   DATE: 02/22/2002
PATENT APPLICATION: US/10/061,727   TIME: 16:08:42

Input Set : A:\3151-A SeqListce 102601.txt
Output Set: N:\CRF3\02222002\J061727.raw

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 3 <110> APPLICANT: Sims, John E.
 4        Smith, Dirk E.
 6 <120> TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
 8 <130> FILE REFERENCE: 3151-A
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/061,727
11 <141> CURRENT FILING DATE: 2001-10-26
13 <150> PRIOR APPLICATION NUMBER: US 60/244,831
14 <151> PRIOR FILING DATE: 2000-10-31
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2064
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(2064)
28 <223> OTHER INFORMATION:
31 <220> FEATURE:
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (1792)..(1792)
34 <223> OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.
37 <400> SEQUENCE: 1
38 atg aca ctt ctg tgg tgt gta gtg agt ctc tac ttt tat gga atc ctg      48
39 Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
40 1               5                   10                  15
42 caa agt gat gcc tca gaa cgc tgc gat gac tgg gga cta gac acc atg      96
43 Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
44             20                  25                  30
46 agg caa atc caa gtg ttt gaa gat gag cca gct cgc atc aag tgc cca     144
47 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
48          35                  40                  45
50 ctc ttt gaa cac ttc ttg aaa ttc aac tac agc aca gcc cat tca gct     192
51 Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
52       50                  55                  60
54 ggc ctt act ctg atc tgg tat tgg act agg cag gac cgg gac ctt gag     240
55 Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
56 65                  70                  75                  80
58 gag cca att aac ttc cgc ctc ccc gag aac cgc att agt aag gag aaa     288
59 Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
60                  85                  90                  95
62 gat gtg ctg tgg ttc cgg ccc act ctc ctc aat gac act ggc aac tat     336
63 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
```

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Input Set : A:\3151-A SeqListce 102601.txt
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64           100                105                110
66 acc tgc atg tta agg aac act aca tat tgc agc aaa gtt gca ttt ccc      384
67 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
68           115                120                125
70 ttg gaa gtt gtt caa aaa gac agc tgt ttc aat tcc ccc atg aaa ctc      432
71 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
72           130                135                140
74 cca gtg cat aaa ctg tat ata gaa tat ggc att cag agg atc act tgt      480
75 Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
76 145                150                155                160
78 cca aat gta gat gga tat ttt cct tcc agt gtc aaa ccg act atc act      528
79 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
80                165                170                175
82 tgg tat atg ggc tgt tat aaa ata cag aat ttt aat aat gta ata ccc      576
83 Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
84                180                185                190
86 gaa ggt atg aac ttg agt ttc ctc att gcc tta att tca aat aat gga      624
87 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
88           195                200                205
90 aat tac aca tgt gtt gtt aca tat cca gaa aat gga cgt acg ttt cat      672
91 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
92           210                215                220
94 ctc acc agg act ctg act gta aag gta gta ggc tct cca aaa aat gca      720
95 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
96 225                230                235                240
98 gtg ccc cct gtg atc cat tca cct aat gat cat gtg gtc tat gag aaa      768
99 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
100                245                250                255
102 gaa cca gga gag gag cta ctc att ccc tgt acg gtc tat ttt agt ttt     816
103 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
104                260                265                270
106 ctg atg gat tct cgc aat gag gtt tgg tgg acc att gat gga aaa aaa     864
107 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
108                275                280                285
110 cct gat gac atc act att gat gtc acc att aac gaa agt ata agt cat     912
111 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
112           290                295                300
114 agt aga aca gaa gat gaa aca aga act cag att ttg agc atc aag aaa     960
115 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
116 305                310                315                320
118 gtt acc tct gag gat ctc aag cgc agc tat gtc tgt cat gct aga agt     1008
119 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
120                325                330                335
122 gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca     1056
123 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
124                340                345                350
126 gct cca aga tac aca gtg gaa ctg gct tgt ggt ttt gga gcc aca gtc     1104
127 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
128                355                360                365
```

Input Set : A:\3151-A SeqListce 102601.txt
Output Set: N:\CRF3\02222002\J061727.raw

```
      130 ctg cta gtg gtg att ctc att gtt gtt tac cat gtt tac tgg cta gag     1152
      131 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
      132     370                 375                 380
      134 atg gtc cta ttt tac cgg gct cat ttt gga aca gat gaa acc att tta     1200
      135 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
      136 385                 390                 395                 400
      138 gat gga aaa gag tat gat att tat gta tcc tat gca agg aat gcg gaa     1248
      139 Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
      140                 405                 410                 415
      142 gaa gaa gaa ttt gta tta ctg acc ctc cgt gga gtt ttg gag aat gaa     1296
      143 Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
      144                 420                 425                 430
      146 ttt gga tac aag ctg tgc atc ttt gac cga gac agt ctg cct ggg gga     1344
      147 Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
      148                 435                 440                 445
      150 aat aca gtg gaa gca gtt ttt gat ttc att cag aga agc aga agg atg     1392
      151 Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
      152     450                 455                 460
      154 att gtt gtt ctg agc cct gac tat gtg aca gaa aag agc atc agc atg     1440
      155 Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
      156 465                 470                 475                 480
      158 ctg gag ttt aaa ctg ggt gtc atg tgc cag aac tcc att gcc acc aag     1488
      159 Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
      160                 485                 490                 495
      162 ctc att gtg gtt gag tac cgt ccc ctt gag cac ccg cac cca ggc att     1536
      163 Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
      164                 500                 505                 510
      166 ctt cag ctc aaa gag tct gtg tct ttt gtg agc tgg aag gga gaa aag     1584
      167 Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
      168     515                 520                 525
      170 tcc aaa cat tct ggc tct aaa ttc tgg aaa gct ttg cgg ttg gct ctt     1632
      171 Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
      172     530                 535                 540
      174 ccc ctg aga agt ctg agt gcc agt tct ggc tgg aat gag agc tgc tct     1680
      175 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
      176 545                 550                 555                 560
      178 tcc cag tct gac atc agt ctg gat cac gtt caa agg agg aga agt cgt     1728
      179 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
      180                 565                 570                 575
      182 ttg aaa gag ccc cca gaa ctt cag agc tca gag agg gct gca ggt agc     1776
      183 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
      184                 580                 585                 590
W--> 186 cct cca gcc cca ggc nca atg tcc aag cac cga ggg aag tcc tcc gcc     1824
W--> 187 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
      188                 595                 600                 605
      190 acc tgc cgc tgt tgt gtc acc tac tgt gaa gga gag aat cac ctt agg     1872
      191 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
      192     610                 615                 620
      194 aac aag agc cgg gca gag att cat aac cag ccc cag tgg gag aca cac     1920
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Input Set : A:\3151-A SeqListce 102601.txt
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```
195 Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
196 625                 630                 635                 640
198 ctc tgt aag cct gtt ccc caa gag tca gaa act caa tgg ata caa aat     1968
199 Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn
200             645                 650                 655
202 ggc acc aga ttg gaa ccc cct gct ccc cag atc tca gcc ctt gct ctt     2016
203 Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
204             660                 665                 670
206 cat cat ttc acg gac tta tcc aat aac aac gac ttt tat atc cta taa     2064
207 His His Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
208         675                 680                 685
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 687
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (598)..(598)
219 <223> OTHER INFORMATION: The 'Xaa' at location 598 stands for Thr or Pro.
221 <400> SEQUENCE: 2
223 Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
224 1               5                   10                  15
227 Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
228             20                  25                  30
231 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
232         35                  40                  45
235 Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
236     50                  55                  60
239 Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
240 65                  70                  75                  80
243 Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
244             85                  90                  95
247 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
248             100                 105                 110
251 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
252         115                 120                 125
255 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
256     130                 135                 140
259 Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
260 145                 150                 155                 160
263 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
264             165                 170                 175
267 Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
268             180                 185                 190
271 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
272         195                 200                 205
275 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
276     210                 215                 220
279 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
```

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PATENT APPLICATION: US/10/061,727

DATE: 02/22/2002
TIME: 16:08:42

Input Set : A:\3151-A SeqListce 102601.txt
Output Set: N:\CRF3\02222002\J061727.raw

```
280 225                     230                 235                      240
283 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
284                 245                 250                 255
287 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
288                 260                 265                 270
291 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
292             275                 280                 285
295 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
296         290                 295                 300
299 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
300 305                 310                 315                 320
303 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
304                 325                 330                 335
307 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
308                 340                 345                 350
311 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
312         355                 360                 365
315 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
316         370                 375                 380
319 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
320 385                 390                 395                 400
323 Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
324                 405                 410                 415
327 Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
328                 420                 425                 430
331 Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
332             435                 440                 445
335 Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
336         450                 455                 460
339 Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
340 465                 470                 475                 480
343 Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
344             485                 490                 495
347 Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
348             500                 505                 510
351 Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
352         515                 520                 525
355 Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
356         530                 535                 540
359 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
360 545                 550                 555                 560
363 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
364             565                 570                 575
367 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
368         580                 585                 590
W--> 371 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
372         595                 600                 605
375 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
376     610                 615                 620
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VERIFICATION SUMMARY　　　　　　　　　 DATE: 02/22/2002
PATENT APPLICATION:　US/10/061,727　　　　TIME: 16:08:43

Input Set : **A:\3151-A SeqListce 102601.txt**
Output Set: **N:\CRF3\02222002\J061727.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2